PCR) and further confirmed by sequence analysis of each amplified PCR product. The data of phylogenetic analyses for these amplified DNA fragments further supported concurrent infections by two or three dengue virus serotypes. Our report suggests that continued dengue surveillance must be designed so as to be acutely sensitive to the detection of multiple dengue virus serotypes by RT-PCR.

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## IDENTIFICATION OF DENGUE SEROTYPES ALONG THE THAI-LAOS BORDER USING THE NASBA TECHNIQUE

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In this study, dengue serotypes were detected by NASBA technique. The samples were 402 probable DF/DHF patients and 171 students, aged 5-15 years old and living in Nhong Kai, Nakhorn Phanom, and Mukdahan provinces. Data were collected from June to September 2002. The samples were tested by Combo Q Check test kit, enzyme-linked immunosorbent assay (ELISA), polymerase chain reaction (PCR), and nucleic acid sequence-based amplification (NASBA). Descriptive statistics, Cochran's Q test, McNemar test, and Kappa were used for statistical analysis. Four serotypes of dengue virus were found in 2 provincial hospitals, except in Mukdahan Provincial Hospital, where only dengue virus serotype 2 was detected by PCR and NASBA. There was excellent correlation in determining dengue serotypes between PCR and NASBA (Cochran's Q test, P = 0.0065, N =75), while the positive cases determined by ELISA were more than those determined by Combo Q Check test (McNemar test, P = 0.02, N = 78). Compared to the PCR method, the sensitivities of NASBA by dengue 1-4 were 100, 100, 88.89, and 100%, respectively, while the specificities of NASBA by dengue 1-4 were 100, 99.32, 100 and 100%, respectively. For serotyping, NASBA showed similar specificity and sensitivity to PCR ($\kappa = 0.97$), was rapid, and used only a heating block and water bath. Therefore, the NASBA technique was more suitable in the field than PCR. (ACMCIP abstract)

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